

### REMARKS AND ELECTION

Claims 1–28 are pending in this application. Claim 24 has been amended herein to correct claim dependency.

In the Office Action dated March 23, 2005, claims 1–28 have been restricted into five groups numbered I to V under the unity of invention criteria of PCT Rule 13.1. The Office Action states that claims 24 and 28 were not included in the restriction because claim 24 depends from a non-existent claim 34 (and claim 28 depends from claim 24). Claim 24 has been amended herein to depend from claim 23. Accordingly, claims 24 and 28 have been included with the claims of Group I below.

In response to the Restriction Requirement, Applicants elect the claims of Group 1 (claims 1-5, 8-10, 14-18, 23-25 and 28; isolated polynucleotides, etc.) with traverse.

The Office Action further requires an election of species; specifically, election of a particular polynucleotide sequence. Applicants elect SEQ ID NO:1 (claims 1(a)(c)(d), 2, 3, 5, 8-10, 14-18, 23-25 and 28) as a species. This election of species is made without traverse to the extent it is understood that, upon the finding of an allowable species, examination will continue with the non-elected species until all species have been examined or a non-allowable species is identified.

The traversal of the restriction is on the basis that the claims of Groups I – V are linked by a single general inventive concept under PCT Rule 13.1. In particular, the claims of Groups I - V are joined by the unifying inventive concept of the DsrA polynucleotides. This unifying feature is novel over the art.

The Restriction Requirement states that:

The special technical feature of the first claimed product of invention I is an isolated polynucleotide that hybridizes to a DNA having the nucleotide sequence of SEQ ID NO:1 **under stringent conditions**. However, such a polynucleotide was already known in the art at the time of the instant invention. For instance, Fleischmann et al., (*Science* 269:496-512) taught an isolated gene

comprising the nucleotide sequence  
CGCACCTTTAACGGCTTAATTTTAGAACATTTAGAA encoding  
DsrA, ArgThrPheAsnGlyLeulleLeuGluHisLeuGlu (see attached  
sequence alignment report). This prior art nucleotide is expected to  
hybridize with the instantly recited SEQ ID NO:1 at least under low  
stringency conditions. Therefore, the special technical features  
of invention 1 does not define over the prior art.

(Office Action, paragraph spanning pages 2-3, emphasis added).

Applicants respectfully note that this discussion is incorrect. The  
sequence from Fleischmann et al. does not encode a DsrA. The cited  
sequence is a portion of the *H. influenzae* strain Rd KW20 gene that  
corresponds to the downstream gene from DsrA in *H. ducreyi* and is a putative  
hemolysin and likely a transmembrane protein. Thus, the Fleischmann et al.  
sequence is not a DsrA coding sequence at all. A BLAST search between the  
*H. ducreyi* DsrA open reading frame (SEQ ID NO:1) versus the complete  
database of *H. influenza* strain Rd KW20 studied by Fleischmann et al. finds no  
*H. influenza* genes with substantial similarity to DsrA. Thus, the evidence to  
date supports the proposition that *H. influenza* does not have a DsrA gene at  
all.

Further, the Office Action states that the sequence of Fleischmann et al.  
is expected to hybridize with the instantly recited SEQ ID NO:1 at least under  
low stringency conditions." Claim 1(c) specifically recites polynucleotide  
sequences that hybridize to the polynucleotides of claim 1(a) and (b) "under  
stringent conditions and which encode DsrA." The Fleischmann et al.  
sequence would not hybridize to SEQ ID NO:1 under stringent conditions and,  
moreover, does not encode a DsrA. If, for the sake of argument, the cited  
Fleischmann et al. sequence hybridizes to SEQ ID NO:1 under low stringency  
conditions is irrelevant to the claimed invention. Given the low degree of  
sequence similarity between SEQ ID NO:1 and the sequence of Fleischmann


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et al., the two sequences would not hybridize to each other under high stringency conditions as recited by claim 1.

Thus, the claims of Groups I – V are linked by DsrA as a common technical feature. This unifying feature is not disclosed by the cited Fleischmann et al. reference. Accordingly, Applicants respectfully submit that Groups I – V should be examined concurrently.

In view of the foregoing, Applicants respectfully request that the Examiner reconsider and withdraw the outstanding Restriction Requirement. This application is in condition for substantive examination, which action is respectfully requested.

Respectfully submitted,

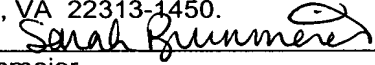
  
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